

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lu, Kuang-hui
Pang, Kevin

(ii) TITLE OF INVENTION: Methods and Reagents for Treating
Glucose Metabolic Disorders

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Foley, Hoag & Eliot
- (B) STREET: One Post Office Square
- (C) CITY: Boston
- (D) STATE: MA
- (E) COUNTRY: USA
- (F) ZIP: 02109

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: ASCII (text)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: 10-FEB-2000
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Vincent, Matthew P.
- (B) REGISTRATION NUMBER: 36,709
- (C) REFERENCE/DOCKET NUMBER: ONV-058.01

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617) 832-1000
- (B) TELEFAX: (617) 832-7000

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 81..371

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 81..164

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 165..371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGCTTGACC	TGCAGTCAGTG	CAGCCCTGG	GACTTCCCTC	GCCTTCCACC	TCCTGCTCGT	60										
CTGCTTCACA	AGCTATCGCT	ATG	GTG	TTC	GTG	CGC	AGG	CCG	TGG	CCC	GCC	110				
		Met	Val	Phe	Val	Arg	Arg	Pro	Trp	Pro	Ala					
-28		-25									-20					
TTG	ACC	ACA	GTG	CTT	CTG	GCC	CTG	CTC	GTC	CTA	GGG	GCG	CTG	GTC	158	
Leu	Thr	Thr	Val	Leu	Leu	Ala	Leu	Leu	Val	Cys	Leu	Gly	Ala	Leu	Val	
-15			-10								-5					
GAC	GCC	TAC	CCC	ATC	AAA	CCC	GAG	GCT	CCC	GGC	GAA	GAC	GCC	TCG	CCG	206
Asp	Ala	Tyr	Pro	Ile	Lys	Pro	Glu	Ala	Pro	Gly	Glu	Asp	Ala	Ser	Pro	
1				5					10							
GAG	GAG	CTG	AAC	CGC	TAC	TAC	GCC	TCC	CTG	CGC	CAC	TAC	CTC	AAC	CTG	254
Glu	Glu	Leu	Asn	Arg	Tyr	Tyr	Ala	Ser	Leu	Arg	His	Tyr	Leu	Asn	Leu	
15		20					25								30	
GTC	ACC	CGG	CAG	CGG	TAT	GGG	AAA	AGA	GAC	GGC	CCG	GAC	AGG	CTT	CTT	302
Val	Thr	Arg	Gln	Arg	Tyr	Gly	Lys	Arg	Asp	Gly	Pro	Asp	Arg	Leu	Leu	
35				40											45	
TCC	AAA	ACG	TTC	TTC	CCC	GAC	GGC	GAG	GAC	CGC	CCC	GTC	AGG	TCG	CGG	350
Ser	Lys	Thr	Phe	Phe	Pro	Asp	Gly	Glu	Asp	Arg	Pro	Val	Arg	Ser	Arg	
50					55				60							
TCG	GAG	GGC	CCA	GAC	CTG	TGG	TGAGGACCCCC	TGAGGCCTCC	TGGGAGATCT							401
Ser	Glu	Gly	Pro	Asp	Leu	Trp										
65																
GCCAACCACG	CCCACGTCA	T	TGCA	TAC	GC	ACT	CCC	GACC	CC	AGAA	ACCC	GG	ATT	CTG	CC	461
TCCCGACGGC	GGCGTCTGGG	CAGGGTT	CGG	GTG	CGG	CC	CG	CC	GT	CTC	GGT	GCC				521
CCGCC	CCC	CTG	GGCT	GGAGGG	CTG	TGT	TGT	GG	TC	CTT	CC	CTG				581
T																582

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Phe	Val	Arg	Arg	Pro	Trp	Pro	Ala	Leu	Thr	Thr	Val	Leu	Leu	
-28		-25											-15			
Ala	Leu	Leu	Val	Cys	Leu	Gly	Ala	Leu	Val	Asp	Ala	Tyr	Pro	Ile	Lys	
				-10		-5						1				
Pro	Glu	Ala	Pro	Gly	Glu	Asp	Ala	Ser	Pro	Glu	Glu	Leu	Asn	Arg	Tyr	
5					10				15					20		
Tyr	Ala	Ser	Leu	Arg	His	Tyr	Leu	Asn	Leu	Val	Thr	Arg	Gln	Arg	Tyr	
				25				30						35		
Gly	Lys	Arg	Asp	Gly	Pro	Asp	Arg	Leu	Leu	Ser	Lys	Thr	Phe	Phe	Pro	
				40				45					50			

Asp Gly Glu Asp Arg Pro Val Arg Ser Arg Ser Glu Gly Pro Asp Leu
55 60 65

Trp